

ID NEK1_HUMAN STANDARD; PRT; 1258 AA.
 AC Q96PY6; Q9Y594;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase NEK1 (EC 2.7.1.37) (NimA-related
 DE protein kinase 1) (NY-REN-55 antigen).
 GN NEK1 OR KIAA1901.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=21456161; PubMed=11572484;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXI.
 RT The complete sequences of 60 new cDNA clones from brain which code for
 RT large proteins.";
 RL DNA Res. 8:179-187(2001).
 RN [2]
 RP SEQUENCE OF 444-1258 FROM N.A. (ISOFORM 2).
 RC TISSUE=Renal cell carcinoma;
 RX MEDLINE=99438124; PubMed=10508479;
 RA Scanlan M.J., Gordan J.D., Williamson B., Stockert E., Bander N.H.,
 RA Jongeneel C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 RA Old L.J.;
 RT "Antigens recognized by autologous antibody in patients with
 RT renal-cell carcinoma.";
 RL Int. J. Cancer 83:456-464(1999).
 CC -!- FUNCTION: PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS
 CC TO POSSESS TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF
 CC MEIOSIS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q96PY6-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q96PY6-2; Sequence=VSP_004870;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. NIMA
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AB067488; BAB67794.1; ALT_INIT.
 DR EMBL; AF155113; AAD42879.1; -.
 DR Genew; HGNC:7744; NEK1.
 DR MIM; 604588; -.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;
 KW Nuclear protein; Phosphorylation; Cell cycle; Cell division;
 KW Tyrosine-protein kinase; Alternative splicing.
 FT DOMAIN 4 258 PROTEIN KINASE.
 FT NP_BIND 10 18 ATP (BY SIMILARITY).
 FT BINDING 33 33 ATP (BY SIMILARITY).
 FT ACT_SITE 128 128 BY SIMILARITY.
 FT VARSPLOC 478 521 Missing (in isoform 2).
 FT /FTid=VSP_004870.
 FT CONFLICT 1232 1232 G -> E (IN REF. 2).
 SQ SEQUENCE 1258 AA; 142828 MW; 339C4BFA56612530 CRC64;
 MEKYVRLQKI GEGSFGKAIL VKSTEDGRQY VIKENISRM SSKEREESRR EVAVLANMKH
 PNIVQYRESF EENGSLYIVM DYCEGGDLFK RINAQKGVLF QEDQILDWV QICLALKHVH
 DRKILHRDIK SQNIFLTKDG TVQLGDFGIA RVLNSTVELA RTCIGTPYYL SPEICENKPY
 NNKSDIWALG CVLYELCTLK HAFEAGSMKN LVLKIISGSF PPVSLHYSYD LRLSVSQLFK
 RNPRDRPSVN SILEKGFIK RIEKFLSPQL IAEEFCLKTF SKFGSQPIPA KRPASGQNSI
 SVMPAQKITK PAAKYGIPLA YKKYGDKKLH EKKPLQKHQ AHQTPEKRVN TGEERRKISE
 EAARKRRLEF IEKEKKQKDQ IISLMKAEQM KRQEKERLER INRAREQGWR NVLSAGGSGE
 VKAPFLGSGG TIAPSSFSSR GQYEHYHAIF DQMQQQRAED NEAKWKREIY GRGLPERGIL
 PGVRPGFPYG AAGHHHFPDA DDIRKTLKRL KAVSKQANAN RQKGQLAVER AKQVEEFLQR
 KREAMQNKAR AEGHMYLAR LRQIRLQNFN ERQIQAKLR GEKKEANHSE GQEGSEEDM
 RRKKIESLKA HANARAAVLK EQLERKRKEA YEREKKVWEE HLVAKGVKSS DVSPPLGQHE
 TGGSPSKQQM RSVISVTSAL KEVGVDSSTL DTRETSEEMQ KTNNAISSKR EILRRLNENL
 KAQEDEKKGQ NLSDTFEINV HEDAKEHEKE KSVSSDRKKW EAGGQLVIPL DELTLDTSFS
 TTERHTVGEV IKLGPNNGSPR RAWGKSPTDS VLKILGEAEL QLQTELENT TIRSEISPEG
 EKYKPLITGE KKVQCISHEI NPSAIVDSPV ETKSPEFSEA SPQMSLKLEG NLEEPDDLET
 EILQEPSGTN KDESLPCTIT DVWISEEKET KETQSADRIT IQENEVSSEDG VSSTVDQLSD
 IHIEPGTND S QHSKCDVDKS VQPEPFFHKV VHSEHLNLVP VQSVQCSPE ESFAFRSHSH
 LPPKNKNKNS LLIGLSTGLF DANNPKMLRT CSLPDLKLF RTLM DVPTVG DVRQDNLEID
 EIEDENIKEG PSDSEDIVFE ETDTDLQELQ ASMEQLLREQ PGEEYSEEEE SVLKNSDVEP
 TANGTDVADE DDNPSSSAL NEEWHS DNSD GEIASECECD SVFNHLEELR LHLEQEMGFE
 KFFEVEYKIK AIHEDEDENI EICSKIVQNI LGNEHQHLYA KILHLVMADG AYQEDNDE

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